```
=============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2011; month=1; day=31; hr=15; min=51; sec=38; ms=517; ]
=============================================================


*************************************************************
Reviewer Comments:
<210>   9
<211>   1743
<212>   PRT
<213>   Escherichia coli


<400>   9


(errored portion shown below)


Gly Ser  Val Ala Asn Glu Glu  Asn Thr Ile Ser Val  Gly Ser Ser


    1550                 1555                 1560


Please remove the blank line between the above amino acid numbers and
their respective amino acids.  Amino acid numbers must appear directly
below their amino acids. Please ensure that the amino acid numbers are
properly aligned (do not use TAB codes between amino acid numbers:  TABs
cause misalignment).


<210>   10
<211>   4684
<212>   PRT
<213>   Escherichia coli


<400>   10


(errored portions shown below)


Ala Asp  Gly Lys Thr Ala Gly  Asn Thr Ala Lys Ala  Tyr Met Ser
```

```
        1595                    1600                    1605
```

Please remove the blank line between the above amino acid numbers and their respective amino acids.

(also in Sequence 10)
Asn Leu  Thr Ala Gly Ser Thr  Asp Ala Val Asn Gly  Ser Gln Leu

```
        3515                    3520                    3525
```

Please remove the blank line between the above amino acid numbers and their amino acids.

<210>   16
<211>   372
<212>   PRT
<213>   Bradorhizobium japonicum

<400>   16

(errored portion shown below)

Ala Leu Ala Ala Ser Ser Leu Gln Phe Asp Pro Arg Pro Gly Lys Ile

```
305                     310                     315                     320
```

Please remove the blank line between the above amino acid numbers and their respective amino acids.


* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

Application No:     10562191          Version No:        3.0


Input Set:


Output Set:


| | |
|---|---|
| **Started:** | 2011-01-21 15:33:41.884 |
| **Finished:** | 2011-01-21 15:33:50.393 |
| **Elapsed:** | 0 hr(s) 0 min(s) 8 sec(s) 509 ms |
| **Total Warnings:** | 44 |
| **Total Errors:** | 8 |
| **No. of SeqIDs Defined:** | 107 |
| **Actual SeqID Count:** | 107 |

| Error code | | Error Description |
|---|---|---|
| W | 402 | Undefined organism found in <213> in SEQ ID (4) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (9) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (10) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (10) |
| W | 402 | Undefined organism found in <213> in SEQ ID (16) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (16) |
| W | 402 | Undefined organism found in <213> in SEQ ID (17) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W | 402 | Undefined organism found in <213> in SEQ ID (29) |
| W | 402 | Undefined organism found in <213> in SEQ ID (31) |
| W | 402 | Undefined organism found in <213> in SEQ ID (36) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (39) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (40) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (41) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (42) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (43) |

```
                    Input Set:


                    Output Set:



                    Started:    2011-01-21 15:33:41.884
                   Finished:    2011-01-21 15:33:50.393
                    Elapsed:    0 hr(s) 0 min(s) 8 sec(s) 509 ms
            Total Warnings:     44
              Total Errors:     8
     No. of SeqIDs Defined:     107
        Actual SeqID Count:     107
```

Error code        Error Description

```
W   213       Artificial or Unknown found in <213>  in SEQ ID (44)

W   213       Artificial or Unknown found in <213>  in SEQ ID (45)

W   213       Artificial or Unknown found in <213>  in SEQ ID (46)

W   213       Artificial or Unknown found in <213>  in SEQ ID (47)

W   213       Artificial or Unknown found in <213>  in SEQ ID (48)

W   213       Artificial or Unknown found in <213>  in SEQ ID (49)

W   402       Undefined organism found in <213>  in SEQ ID (50)

W   402       Undefined organism found in <213>  in SEQ ID (51)

W   213       Artificial or Unknown found in <213>  in SEQ ID (52)

W   402       Undefined organism found in <213>  in SEQ ID (53)

W   402       Undefined organism found in <213>  in SEQ ID (54)

W   402       Undefined organism found in <213>  in SEQ ID (56)

W   402       Undefined organism found in <213>  in SEQ ID (57)

W   402       Undefined organism found in <213>  in SEQ ID (58)

W   402       Undefined organism found in <213>  in SEQ ID (59)

W   402       Undefined organism found in <213>  in SEQ ID (60)

W   402       Undefined organism found in <213>  in SEQ ID (61)

W   402       Undefined organism found in <213>  in SEQ ID (65)

W   402       Undefined organism found in <213>  in SEQ ID (72)

W   402       Undefined organism found in <213>  in SEQ ID (78)

W   402       Undefined organism found in <213>  in SEQ ID (92)
              This error has occured more than 20 times, will not be displayed

W   213       Artificial or Unknown found in <213>  in SEQ ID (106)
```

<110>    MASIGNANI, Vega
         ARICO, Maria Beatrice

<120>    VIRULENCE-ASSOCIATED ADHESINS

<130>    2300-20667

<140>    10562191
<141>    2011-01-21


<150>    PCT/IB2004/002351
<151>    2004-06-25

<150>    GB 0315022.4
<151>    2003-06-26

<160>    107

<170>    PatentIn version 3.5

<210>    1
<211>    223
<212>    PRT
<213>    Haemophilus aegyptius

<400>    1

Met Lys Arg Asn Leu Leu Lys Gln Ser Val Ile Ala Val Leu Ile Gly
1               5                   10                  15


Gly Thr Thr Val Ser Asn Tyr Ala Leu Ala Gln Ala Gln Ala Gln Ala
                20                  25                  30


Gln Val Lys Lys Asp Glu Leu Ser Glu Leu Lys Lys Gln Val Lys Glu
            35                  40                  45


Met Asp Ala Ala Ile Asp Gly Ile Leu Asp Asp Asn Ile Ala Tyr Glu
        50                  55                  60


Ala Glu Val Asp Ala Lys Leu Asp Gln His Ser Ala Ala Leu Gly Arg
65                  70                  75                  80


His Thr Asn Arg Leu Asn Asn Leu Lys Thr Ile Ala Glu Lys Ala Lys
                85                  90                  95


Gly Asp Ser Ser Glu Ala Leu Asp Lys Ile Glu Ala Leu Glu Glu Gln
                100                 105                 110

Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
        115                 120                 125

Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
        130                 135                 140

Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
145                 150                 155                 160

Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
                165                 170                 175

Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
        180                 185                 190

Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
        195                 200                 205

Ala Ala Val Gly Gly Tyr Lys Ser Gln Thr Ala Val Ala Val Gly
        210                 215                 220


<210>   2
<211>   338
<212>   PRT
<213>   Escherichia coli

<400>   2

Met Lys Thr Val Asn Val Ala Leu Leu Ala Leu Ile Ile Ser Ala Thr
1               5                   10                  15

Ser Ser Pro Val Val Leu Ala Gly Asp Thr Ile Glu Ala Ala Ala Thr
            20                  25                  30

Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
        35                  40                  45

Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
        50                  55                  60

Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
65                  70                  75                  80

Thr Gln Thr Pro Thr Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr
                  85                  90                  95

Val Ala Ala Thr Gly Asp Val Gln Thr Thr Ala Arg Tyr Gln Ser Met
              100                 105               110

Ile Asn Ala Arg Gln Ser Ala Val Thr Asp Ala Gln Gln Thr Gln Ile
              115               120               125

Thr Glu Gln Gln Ala Gln Ile Val Ala Thr Gln Lys Thr Leu Ala Ala
    130               135               140

Thr Gly Asp Thr Gln Asn Thr Ala His Tyr Gln Glu Met Ile Asn Ala
145               150               155               160

Arg Leu Ala Ala Gln Asn Glu Ala Asn Gln Arg Thr Ala Thr Glu Gln
              165               170               175

Gly Gln Lys Met Asn Ala Leu Thr Thr Asp Val Ala Val Gln Gln Gln
              180               185               190

Asn Glu Arg Thr Gln Tyr Asp Lys Gln Met Gln Ser Leu Ala Gln Glu
              195               200               205

Ser Ala Gln Ala His Glu Gln Ile Asp Ser Leu Ser Gln Asp Val Thr
    210               215               220

Gln Thr His Gln Gln Leu Thr Asn Thr Gln Lys Arg Val Ala Asp Asn
225               230               235               240

Ser Gln Gln Ile Asn Thr Leu Asn Asn His Phe Ser Ser Leu Lys Asn
              245               250               255

Glu Val Asp Asp Asn Arg Lys Glu Ala Asn Ala Gly Thr Ala Ser Ala
              260               265               270

Ile Ala Ile Ala Ser Gln Pro Gln Val Lys Thr Gly Asp Val Met Met
              275               280               285

Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
    290               295               300

Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile

Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
                    325                 330                 335

Ser Phe


<210>   3
<211>   1588
<212>   PRT
<213>   Escherichia coli

<400>   3

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Asn Tyr
1               5                   10                  15


Thr Val Thr Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
                    20                  25                  30


Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Met Leu Ser Ser
                    35                  40                  45


Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
        50                  55                  60


Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
65              70                  75                  80


Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
                    85                  90                  95


Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
                    100                 105                 110


Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
                    115                 120                 125


Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
                    130                 135                 140


Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
145                 150                 155                 160

```
Lys Leu Ser Ile Ala Met Gly Asp Ser Ser Lys Ala Glu Gly Ala Asn
              165                 170                 175

Ala Ile Ala Leu Gly Asn Ala Thr Lys Ala Thr Glu Ile Met Ser Ile
              180                 185                 190

Ala Leu Gly Asp Thr Ala Asn Ala Ser Lys Ala Tyr Ser Met Ala Leu
              195                 200                 205

Gly Ala Ser Ser Val Ala Ser Glu Glu Asn Ala Ile Ala Ile Gly Ala
              210                 215                 220

Glu Thr Glu Ala Ala Glu Asn Ala Thr Ala Ile Gly Asn Asn Ala Lys
225                 230                 235                 240

Ala Lys Gly Thr Asn Ser Met Ala Met Gly Phe Gly Ser Leu Ala Asp
              245                 250                 255

Lys Val Asn Thr Ile Ala Leu Gly Asn Gly Ser Gln Ala Leu Ala Asp
              260                 265                 270

Asn Ala Ile Ala Ile Gly Gln Gly Asn Lys Ala Asp Gly Val Asp Ala
              275                 280                 285

Ile Ala Leu Gly Asn Gly Ser Gln Ser Arg Gly Leu Asn Thr Ile Ala
              290                 295                 300

Leu Gly Thr Ala Ser Asn Ala Thr Gly Asp Lys Ser Leu Ala Leu Gly
305                 310                 315                 320

Ser Asn Ser Ser Ala Asn Gly Ile Asn Ser Val Ala Leu Gly Ala Asp
              325                 330                 335

Ser Ile Ala Asp Leu Asp Asn Thr Val Ser Val Gly Asn Ser Ser Leu
              340                 345                 350

Lys Arg Lys Ile Val Asn Val Lys Asn Gly Ala Ile Lys Ser Asp Ser
              355                 360                 365

Tyr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Ala Ile Ser Asp Ser Val
              370                 375                 380
```

```
Ala Lys Arg Leu Gly Gly Gly Ala Ala Val Asp Val Asp Asp Gly Thr
385             390             395             400

Val Thr Ala Pro Thr Tyr Asn Leu Lys Asn Gly Ser Lys Asn Asn Val
                405             410             415

Gly Ala Ala Leu Ala Val Leu Asp Glu Asn Thr Leu Gln Trp Asp Gln
            420             425             430

Thr Lys Gly Lys Tyr Ser Ala Ala His Gly Thr Ser Ser Pro Thr Ala
            435             440             445

Ser Val Ile Thr Asp Val Ala Asp Gly Thr Ile Ser Ala Ser Ser Lys
            450             455             460

Asp Ala Val Asn Gly Ser Gln Leu Lys Ala Thr Asn Asp Asp Val Glu
465             470             475             480

Ala Asn Thr Ala Asn Ile Ala Thr Asn Thr Ser Asn Ile Ala Thr Asn
            485             490             495

Thr Ala Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp
            500             505             510

Ser Val Gly Asp Leu Gln Ala Asp Ala Leu Leu Trp Asn Glu Thr Lys
            515             520             525

Lys Ala Phe Ser Ala Ala His Gly Gln Asp Thr Thr Ser Lys Ile Thr
            530             535             540

Asn Val Lys Asp Ala Asp Leu Thr Ala Asp Ser Thr Asp Ala Val Asn
545             550             555             560

Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr
            565             570             575

Asn Ile Ala Asn Asn Thr Ser Asn Ile Ala Thr Asn Thr Thr Asn Ile
            580             585             590

Ser Asn Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys
            595             600             605

Trp Asp Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Thr Glu Thr
```

Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser
625                630                635                640

Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val
645                650                655

Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn
660                665                670

Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp
675                680                685

Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser
690                695                700

Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp
705                710                715                720

Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr
725                730                735

Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly
740                745                750

Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala
755                760                765

Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu
770                775                780

Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn
785                790                795                800

Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp
805                810                815

Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser
820                825                830

Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly
835                840                845

```
Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
    850             855             860

Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
865             870             875             880

Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
            885             890             895

Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
            900             905             910

Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
    915             920             925

Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
    930             935             940

Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
945             950             955             960

Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
            965             970             975

Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
            980             985             990

His Asp Gly Lys Ala Ser Ile Ile  Thr Asn Val Ala Asn  Gly Ser Ile
    995             1000            1005

Ser Glu  Asp Ser Thr Asp Ala  Val Asn Gly Ser Gln  Leu Asn Ala
    1010            1015            1020

Thr Asn  Met Met Ile Glu Gln  Asn Thr Gln Ile Ile  Asn Gln Leu
    1025            1030            1035

Ala Gly  Asn Thr Asp Ala Thr  Tyr Ile Gln Glu Asn  Gly Ala Gly
    1040            1045            1050

Ile Asn  Tyr Val Arg Thr Asn  Asp Asp Gly Leu Ala  Phe Asn Asp
    1055            1060            1065
```

Ala Ser  Ala Gln Gly Val Gly  Ala Thr Ala Ile Gly  Tyr Asn Ser
    1070             1075             1080

Val Ala  Lys Gly Asp Ser Ser  Val Ala Ile Gly Gln  Gly Ser Tyr
    1085             1090             1095

Ser Asp  Val Asp Thr Gly Ile  Ala Leu Gly Ser Ser  Ser Val Ser
    1100             1105             1110

Ser Arg  Val Ile Ala Lys Gly  Ser Arg Asp Thr Ser  Ile Thr Glu
    1115             1120             1125

Asn Gly  Val Val Ile Gly Tyr  Asp Thr Thr Asp Gly  Glu Leu Leu
    1130             1135             1140

Gly Ala  Leu Ser Ile Gly Asp  Asp Gly Lys Tyr Arg  Gln Ile Ile
    1145             1150             1155

Asn Val  Ala Asp Gly Ser Glu  Ala His Asp Ala Val  Thr Val Arg
    1160             1165             1170

Gln Leu  Gln Asn Ala Ile Gly  Ala Val Ala Thr Thr  Pro Thr Lys
    1175             1180             1185

Tyr Phe  His Ala Asn Ser Thr  Glu Glu Asp Ser Leu  Ala Val Gly
    1190             1195             1200

Thr Asp  Ser Leu Ala Met Gly  Ala Lys Thr Ile Val  Asn Gly Asp
    1205             1210             1215

Lys Gly  Ile Gly Ile Gly Tyr  Gly Ala Tyr Val Asp  Ala Asn Ala
    1220             1225             1230

Leu Asn  Gly Ile Ala Ile Gly  Ser Asn Ala Gln Val  Ile His Val
    1235             1240             1245

Asn Ser  Ile Ala Ile Gly Asn  Gly Ser Thr Thr Thr  Arg Gly Ala
    1250             1255             1260

Gln Thr  Asn Tyr Thr Ala Tyr  Asn Met Asp Ala Pro  Gln Asn Ser
    1265             1270             1275

```
Val Gly  Glu Phe Ser Val Gly  Ser Ala Asp Gly Gln  Arg Gln Ile
    1280             1285              1290

Thr Asn  Val Ala Ala Gly Ser  Ala Asp Thr Asp Ala  Val Asn Val
    1295             1300              1305

Gly Gln  Leu Lys Val Thr Asp  Ala Gln Val Ser Gln  Asn Thr Gln
    1310             1315              1320

Ser Ile  Thr Asn Leu Asp Asn  Arg Val Thr Asn Leu  Asp Ser Arg
    1325             1330              1335

Val Thr  Asn Ile Glu Asn Gly  Ile Gly Asp Ile Val  Thr Thr Gly
    1340             1345              1350

Ser Thr  Lys Tyr Phe Lys Thr  Asn Thr Asp Gly Val  Asp Ala Ser
    1355             1360              1365

Ala Gln  Gly Lys Asp Ser Val  Ala Ile Gly Ser Gly  Ser Ile Ala
    1370             1375              1380

Ala Ala  Asp Asn Ser Val Ala  Leu Gly Thr Gly Ser  Val Ala Thr
    1385             1390              1395

Glu Glu  Asn Thr Ile Ser Val  Gly Ser Ser Thr Asn  Gln Arg Arg
    1400             1405              1410

Ile Thr  Asn Val Ala Ala Gly  Lys Asn Ala Thr Asp  Ala Val Asn
    1415             1420              1425

Val Ala  Gln Leu Lys Ser Ser  Glu Ala Gly Gly Val  Arg Tyr Asp
    1430
```